

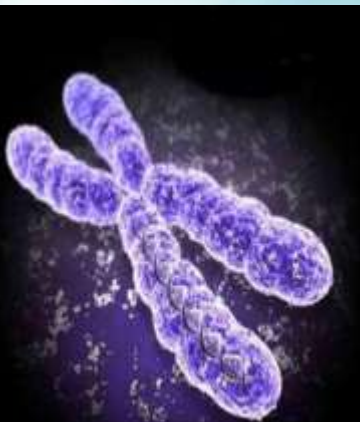
EPIGENETICS AND NEPHROLOGY



Amr Mohab

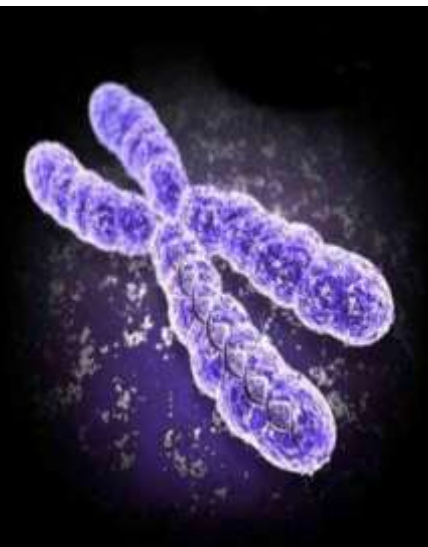
Lecturer of Internal Medicine &
Nephrology Ain Shams University

2015



AGENDA

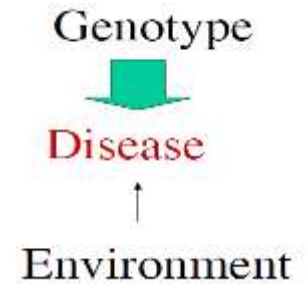
- Basis of genetics
- What is epigenetics?
- Basic epigenetic concepts
- Epigenetic role & applications in Nephrology





Darwin, Mendel, and Lamarck looking sharp portrait style.

Genetics



- Genes control the inheritance of traits (Mendel, 1865)
- The human genome project completed in 2003
- Mutation of a single gene can play a major role in diseases
- Genetics of common, complex traits will provide risk factors = identify people at higher risk



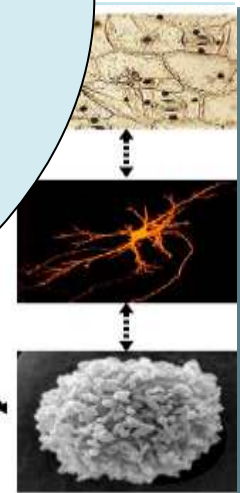
How could you explain?

Identical twins
have different
natural hair
colors?

An Individual with Two
Different

Different adult stem cells
know their fate
Stem cells can only form
Stem cells only form skin

Scientists now know
that genes are not
the only authors of
inheritance. There
are ***ghostwriters***,
too

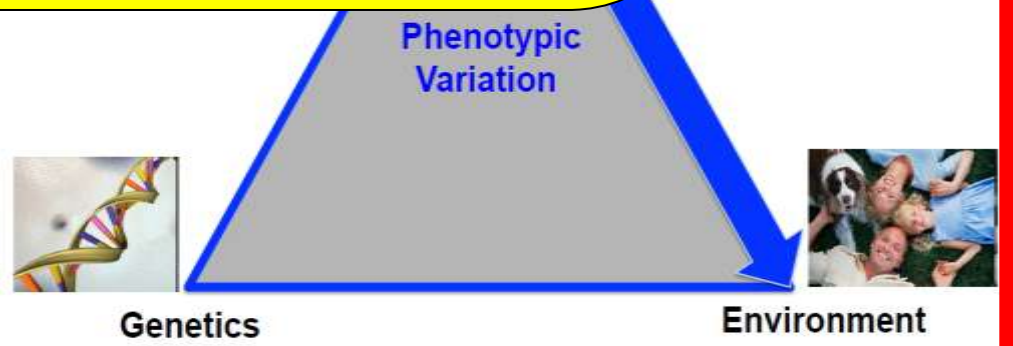


It is Epigenetics not

- ***The rise of epigenetics....*** in the late 20th century was a turning point in our understanding of heredity, as possibly one of the greatest revolution

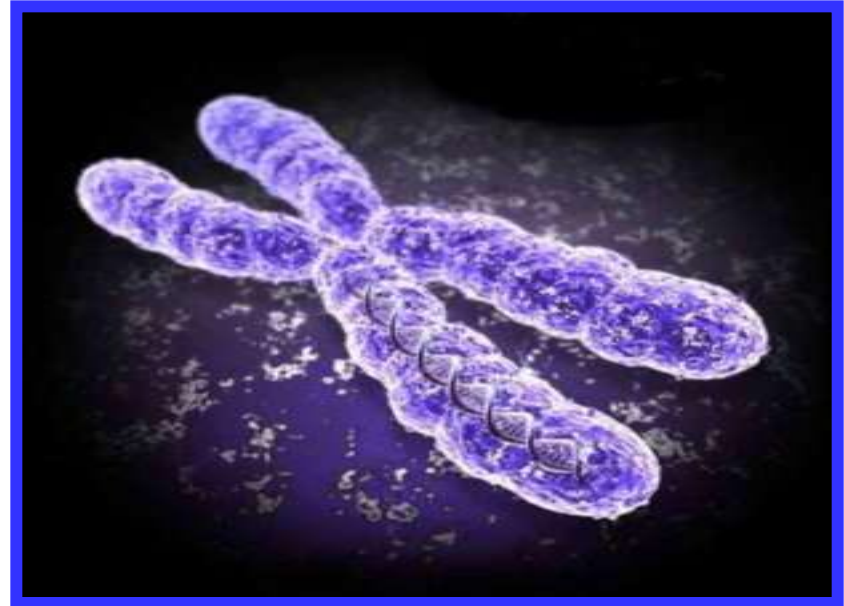
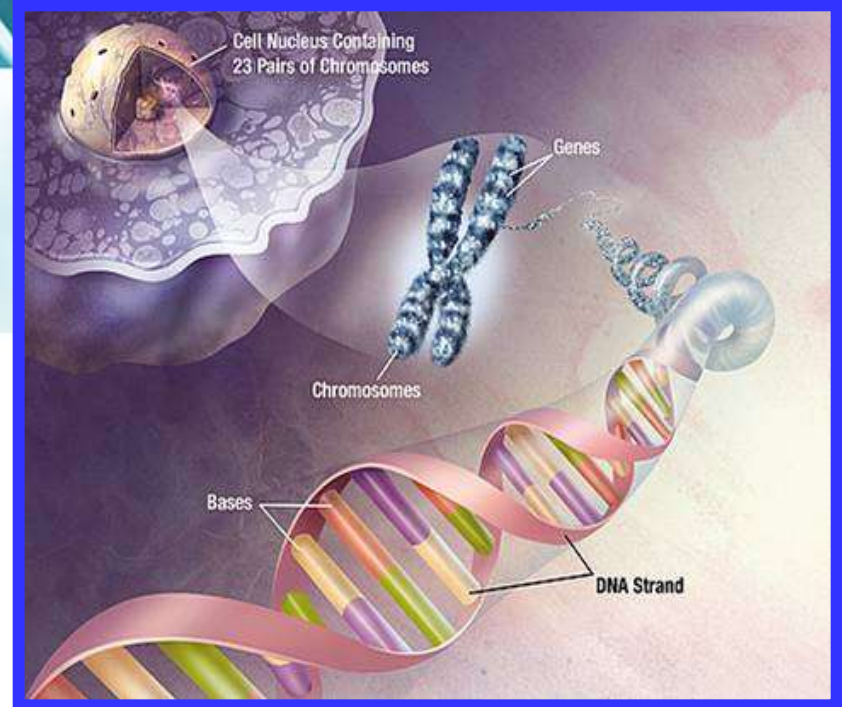


Waddington

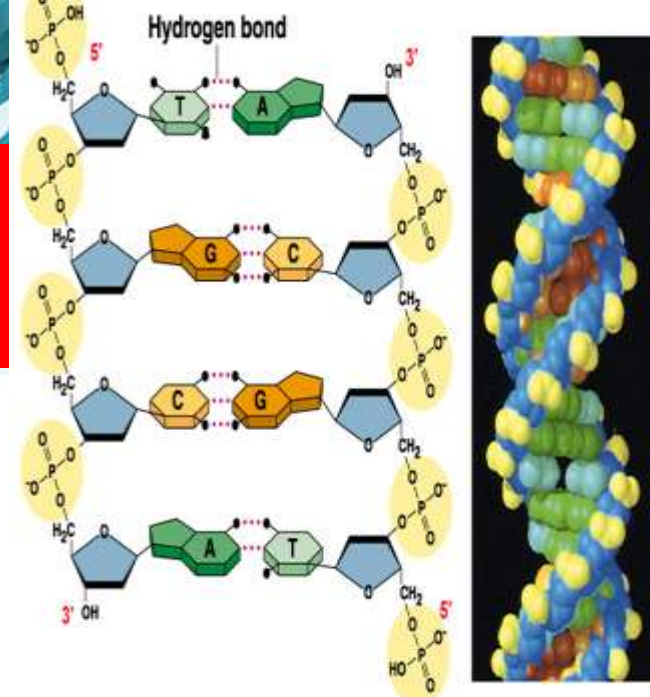


The nucleus

- **Chromosomes**
- **Genes**
- **DNA**



What is DNA?

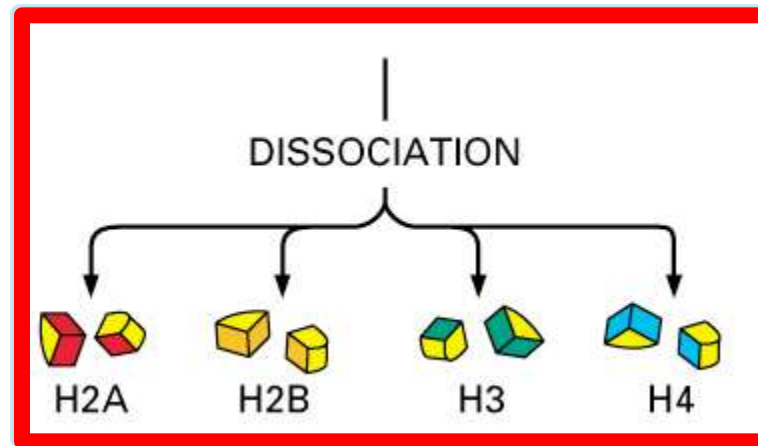
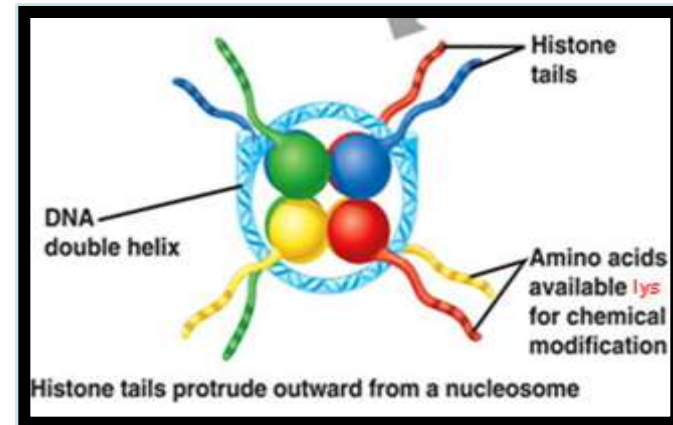
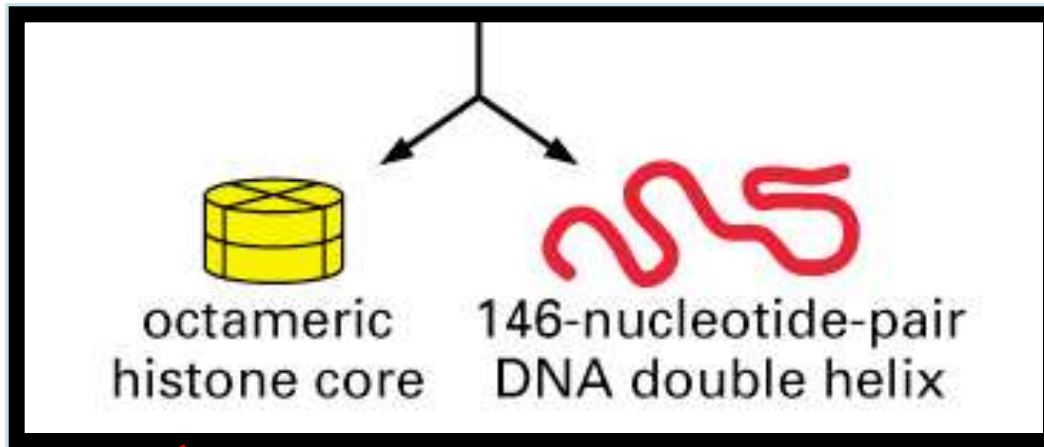


- DNA is a **Double Helix of polynucleotides**
- Each nucleotide consists of: sugar, PO₄ group, nitrogen base (Adenine, Guanine, Thymine, Cytosine)
- **2 m of linear DNA** have to be **packed** into a nucleus of roughly 10 μm diameter
- DNA coils around **8 histone protein cores** forming nucleosomes; the "beads on a string" structure (chromatin).
- Nucleosomes are folded several times to eventually form a chromosome

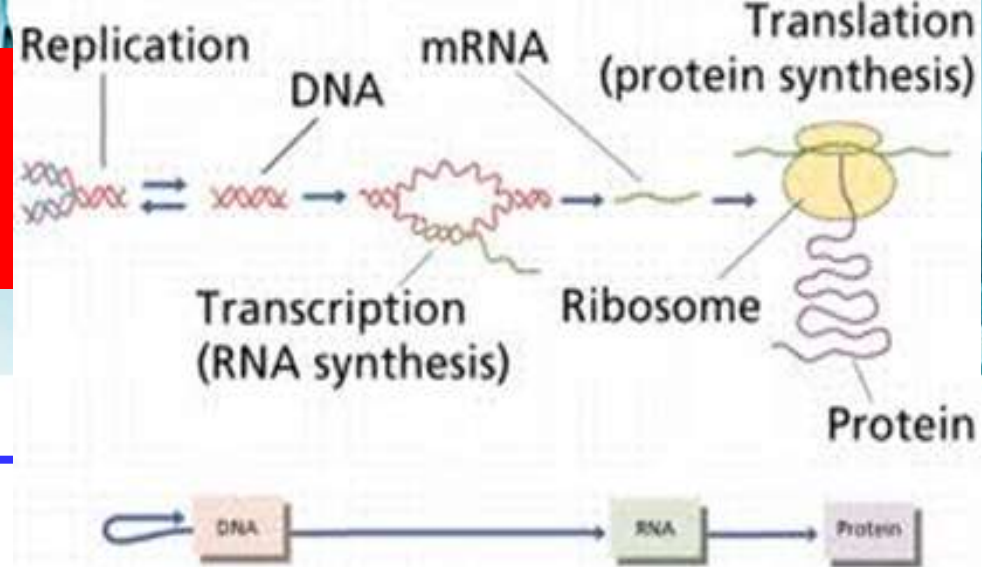
DNA is packaged in nucleosomes

The **nucleosome**

chromatin fiber



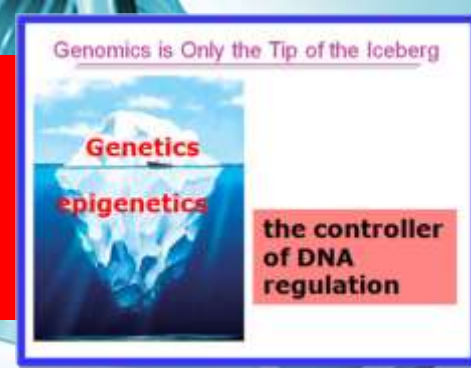
GENETIC CODE



- A gene is a portion of DNA
- The sequence of nucleotides in a gene is read and translated by a cell to produce a chain of amino acids then into proteins this is known as the genetic code
- Conversion of genetic information to a protein relies on the transcription of nucleotide sequences of DNA to mRNA

Genes may be activated or inactivated (silenced), determined by a cell's or environment : by interference with transcription by mRNA, or post translation modification
A Silenced Gene is not Transcribed, Translated, or Expressed

Body cell information



- There are at least 2 forms of information in the genome of the cell:

- A- Genetic information: provides the building block for the manufacture of all Proteins needed for the cell functional activity. Simple genetics based on changes to the DNA sequence (the genotype) 1st Genetic Code
- B- Epigenetic information: provides additional instruction on how, when and where these information should be used, & *decide what happens to genes over course of our life* . 2nd Genetic Code

What does “epigenetics” mean?

= above or on top of genetics

- ❑ While epigenetics often refers to the study of single genes or sets of genes, epigenomics refers to more global analyses of epigenetic changes across the entire **genome**.

- **Who you are is written in both pen and pencil.**
- **Things written in pen you can't change. That's DNA.**
- **But things written in pencil you can. That's epigenetics.**

Every individual has a unique epigenome, even mono-zygotic twin, born with very similar epigenomes but by time are exposed to different environmental factors, their epigenomes differ more and more

The genetic code is unique for each cell type and for each disease

Genetics is the hardware, the epigenetics is the *software*, epigenetics is the genome's operating system

The epigenetic modifications are **dynamic** (vary over time)

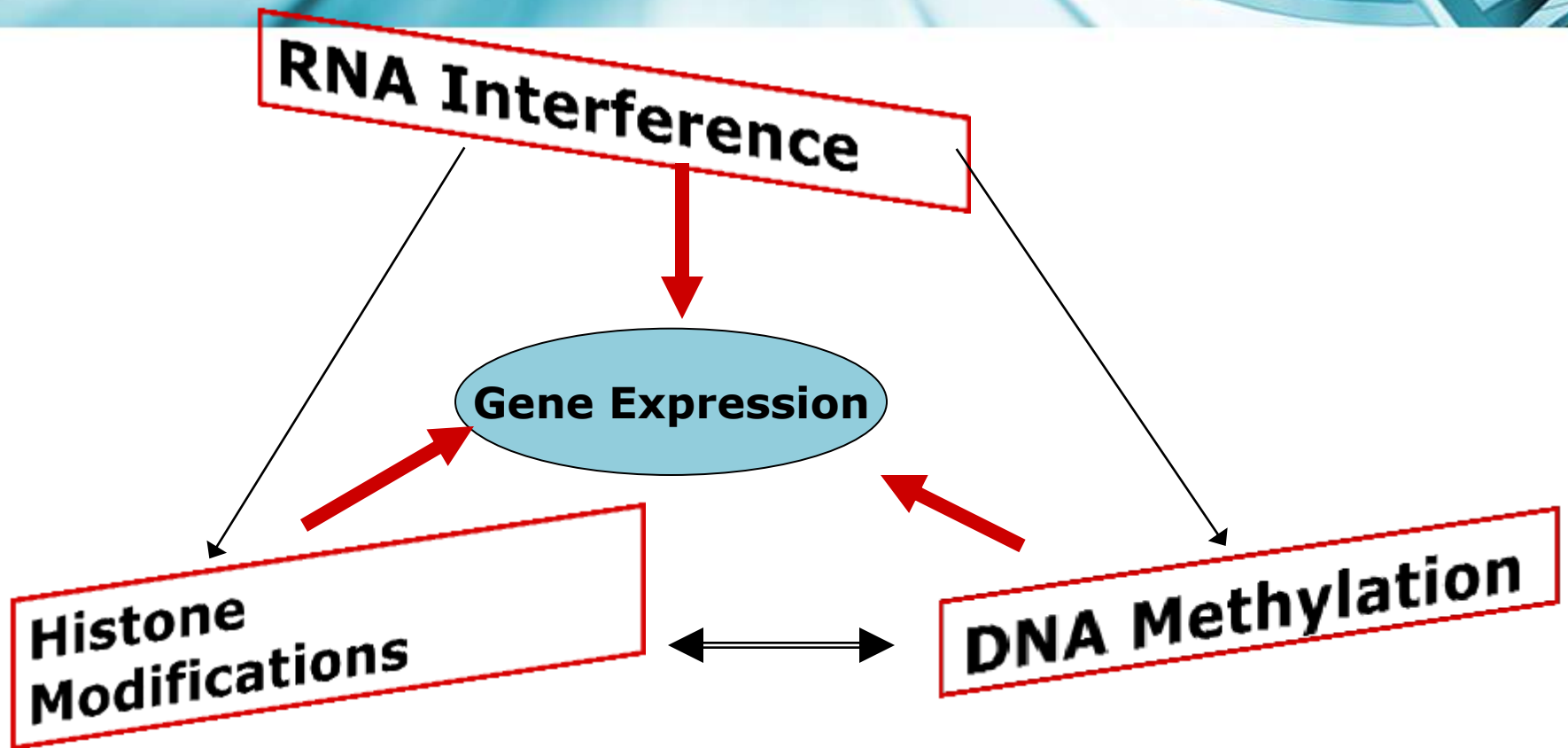
Epigenetic mechanisms are usually reversible

Can be passed down to off springs

Features of epigenetics

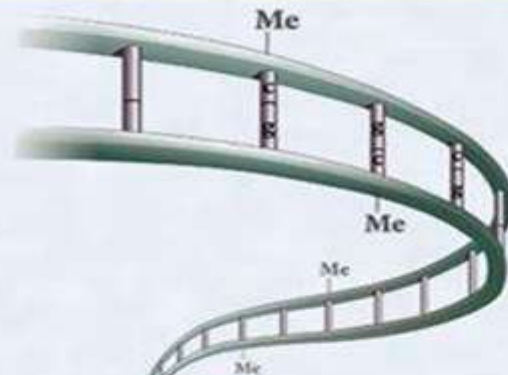
How are epigenetic information accomplished ?

Epigenetics Mechanisms



These heritable modifications are collectively termed
“**epigenetic codes**”

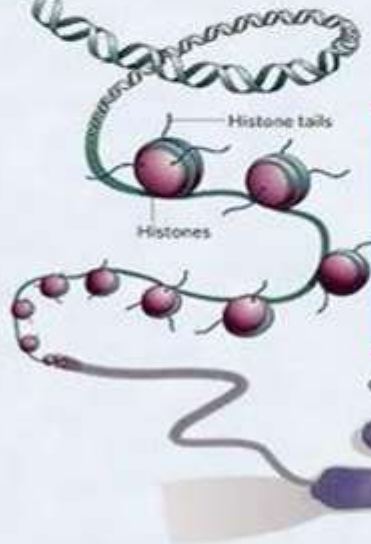
The two main mechanisms of the epigenetic code



The 'epigenetic' code

DNA methylation

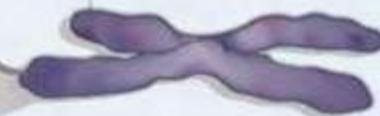
Methyl marks added to certain DNA bases repress gene activity



Histone modification

A combination of different molecules can attach to the "tails" of proteins called histones. These alter the activity of the DNA wrapped around them

Chromosome

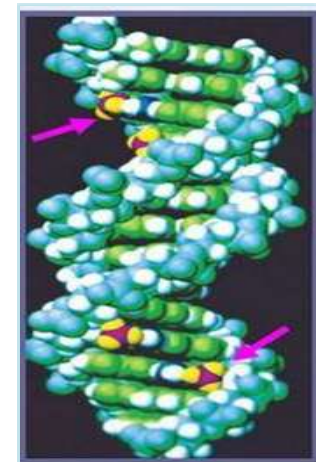
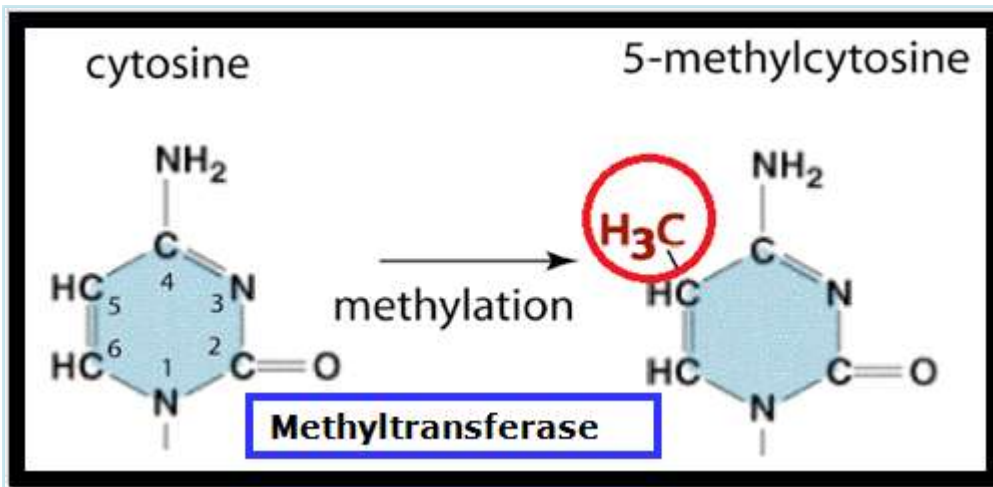


1-DNA Methylation

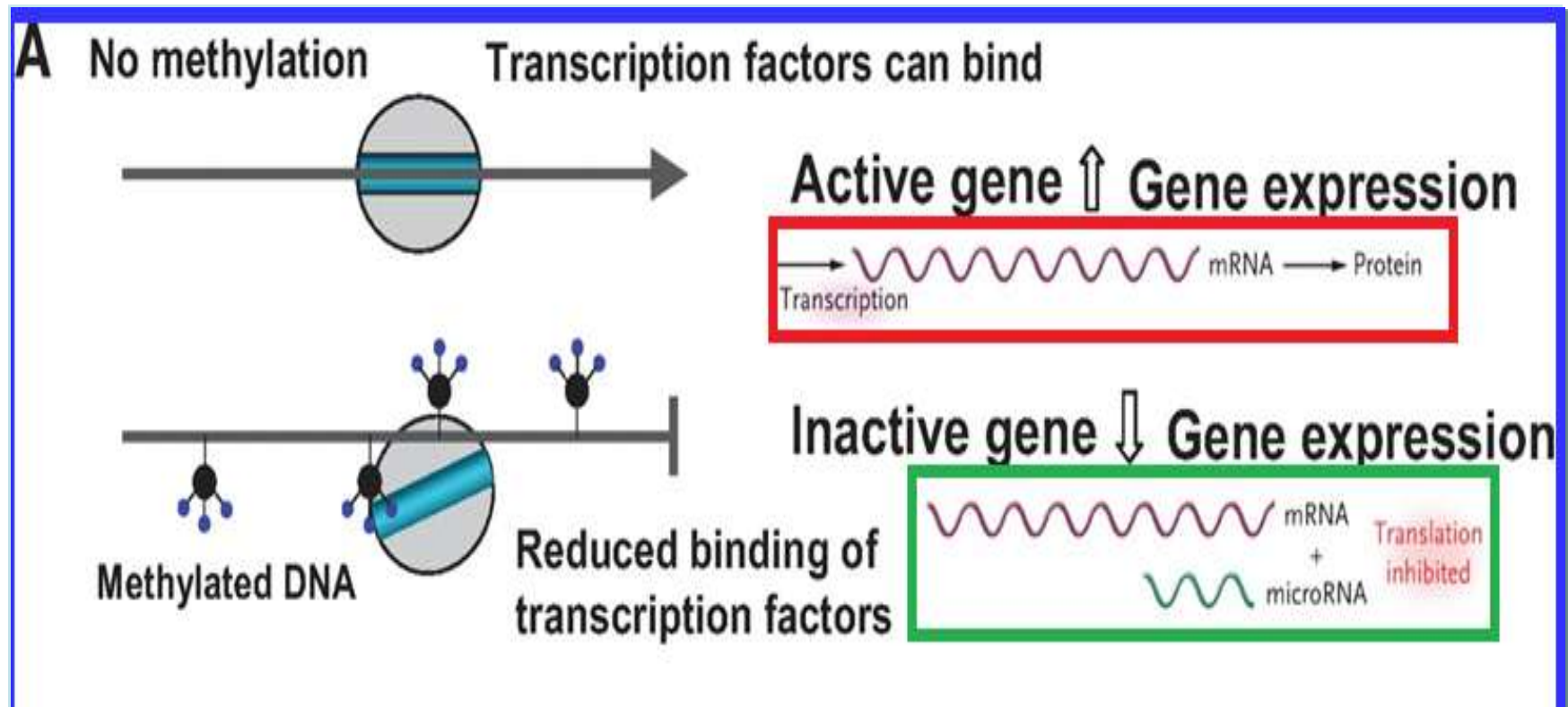
Methyl-
cytosine



- Methylation of cytosine in DNA occurs at CpG dinucleotides is a stable **epigenetic mark**
- DNA methylation is a modification of **DNA that does not change the DNA sequence**, but has an influence on **gene activity** at the level of transcription or translation



EFFECTS OF DNA METHYLATION ON GENE EXPRESSION



What is the effect of DNA methylation

- Methylation affects **gene activity**, keeps the histones tight together so **the DNA cannot be transcribed/expressed**.
- The presence of 5-methylcytosine leads to **the silencing of genes** in that local area of the chromosome = **gene repression**
- This change is **reversible** , making it a **therapeutic target**

Cytosine methylation in mammals

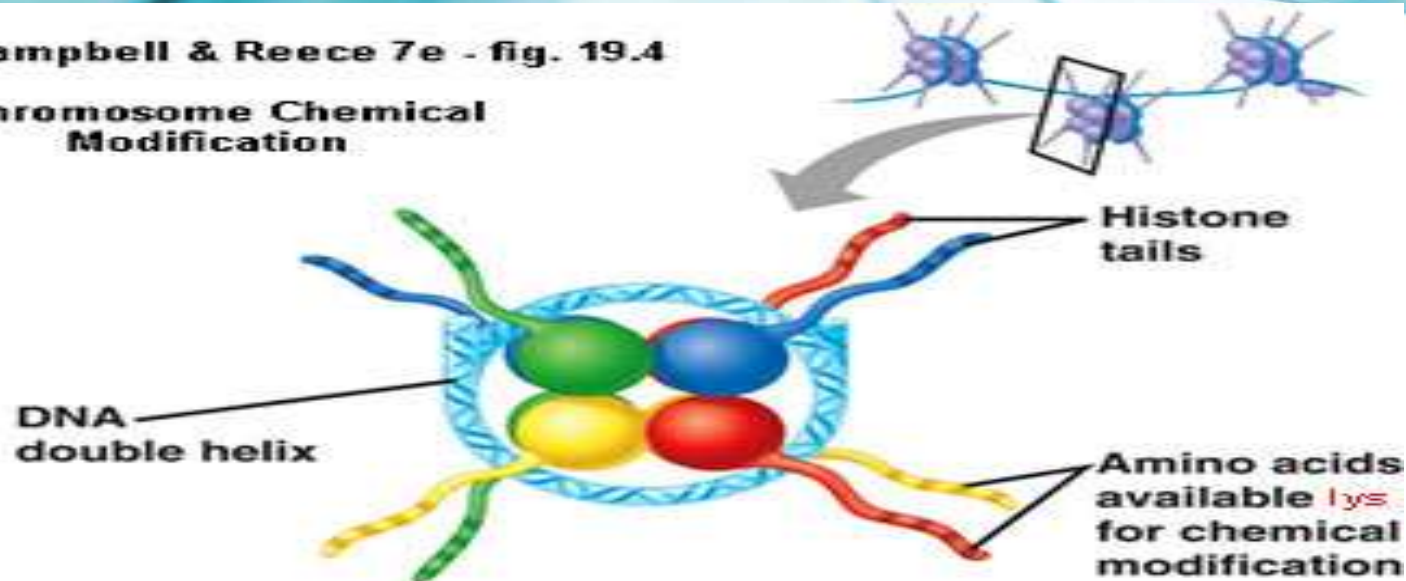
- Gene expression
- Chromosomal stability
- Cell differentiation
- Imprinting
- X-Inactivation
- Carcinogenesis
- Aging



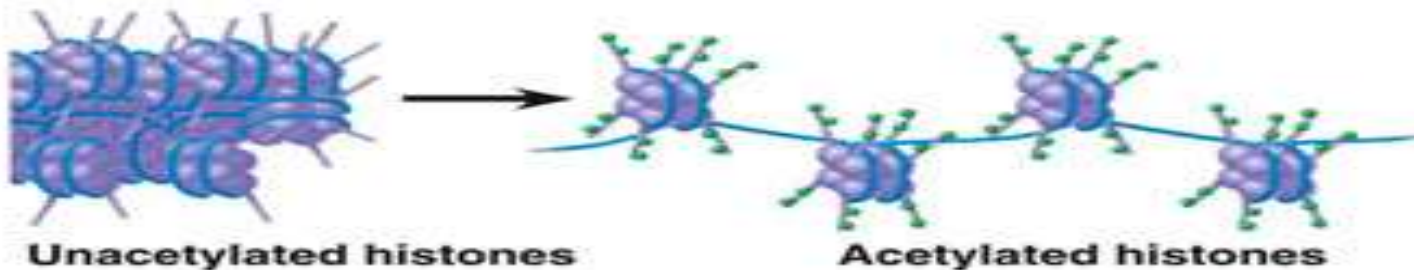
2-Histone Modifications

Campbell & Reece 7e - fig. 19.4

Chromosome Chemical Modification



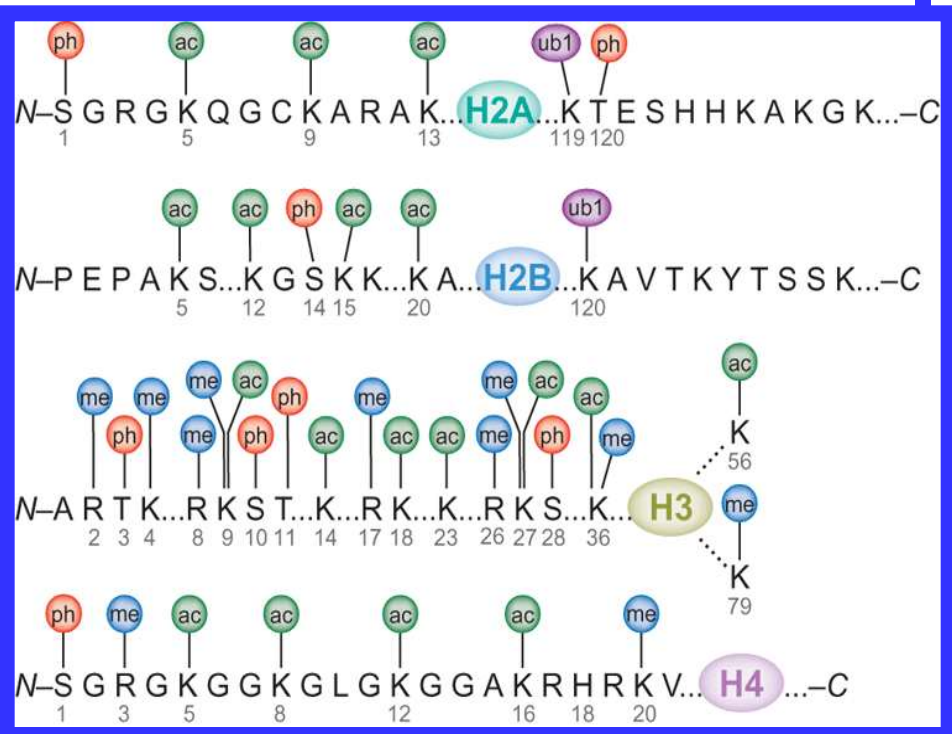
(a) Histone tails protrude outward from a nucleosome



(b) Acetylation of histone tails promotes loose chromatin structure that permits transcription

Histone Modifications

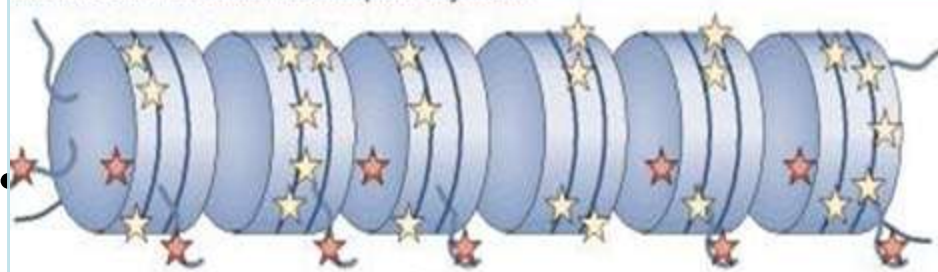
- Histone Tails are subject to a variety of covalent modifications by enzymes
- Acetylation*
- Deacetylation*
- Methylation*
- Demethylation*
- Phosphorylation*



“Histone Code” hypothesis

Medscape

Condensed chromatin: transcriptionally inert



Epigenetic marks:

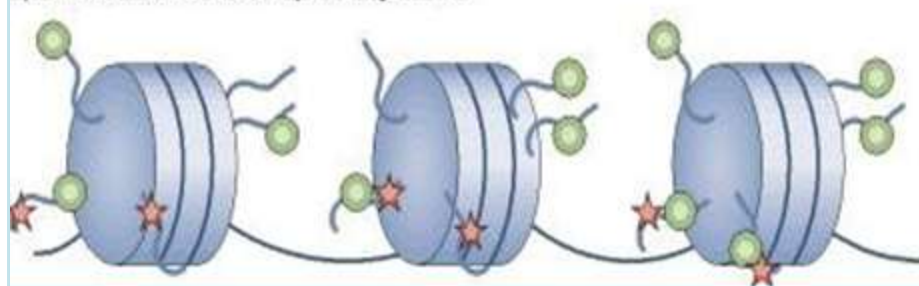
DNA: Hypermethylation at CpG sites

Histones: Hypoacetylation
 Methylation H3K9, H3K27, H4K20

HATs
HMTs
DMs

HDACs
DNMTs
HMTs
DMs

Open chromatin: transcriptionally active



Epigenetic marks:

DNA: Hypomethylation at CpG sites

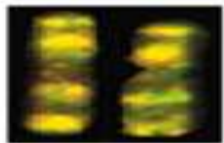
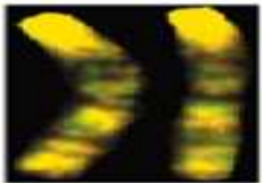
Histones: Hyperacetylation
 Methylation H3K4, H3K36, H4K79

Source: Nat Rev Urol © 2010 Nature Publishing Group

Epigenetic differences arise during the lifetime of monozygotic twins

- Identical twins may have a different methylation pattern
- Epigenetic Factors Can Explain Susceptibility to Illness

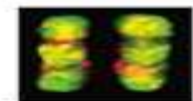
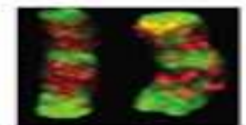
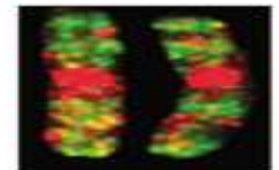
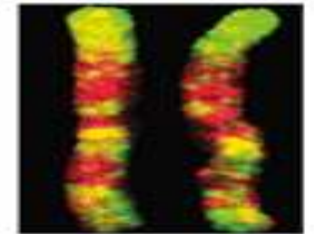
3-year-old twins



very similar
distribution of
DNA
methylation
indicated by the
presence of the
yellow color
obtained by
equal amounts
of
the green and
red dyes

abundant
changes in the
pattern of DNA
methylation
observed by the
presence of
green and red
signals that
indicate
hypermethylation
and
hypomethylation
events

50-year-old twins

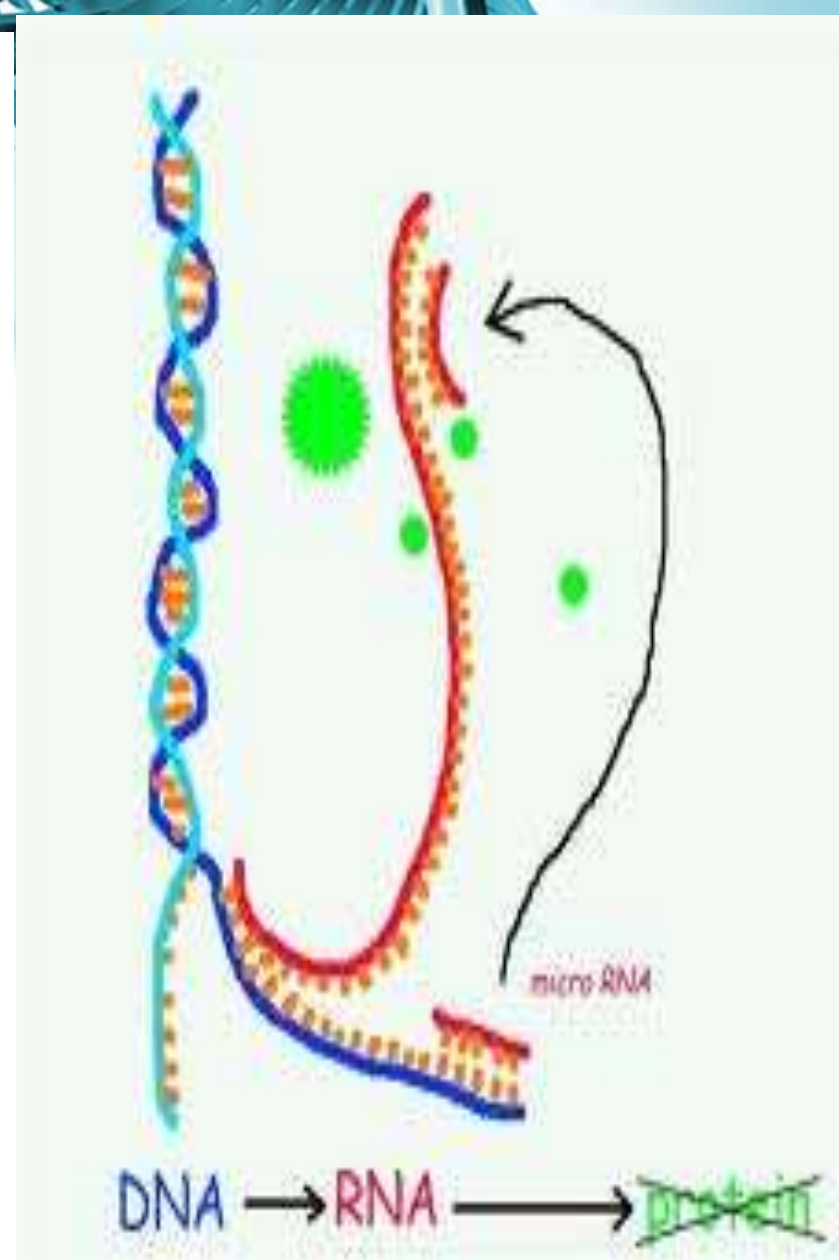


3-Micro RNA(miRNA) or small interfering RNA (siRNA)

- miRNAs are endogenously expressed 18-24 nucleotide single strand small non coding RNA molecules that principally function by binding to the 3' untranslated region of mRNA and repress the expression of their gene products (at transcriptional and post transcriptional levels). **Lee RC, et al 1993**
- Unlike small interfering RNAs in plants , animal miRNA don't require complete complementarity to bind their targets. Thus one miRNA can regulate multiple mRNAs and one mRNA can be repressed by different miRNAs.

He L, Hannon GJ. 2004

- ❑ Expression of miRNAs is altered in many pathophysiologic conditions and regulation of miRNAs by drugs is essential for drug activity.
- ❑ Several miRNAs circulate in the blood and can be used as biological markers for diagnosis and prognosis of specific cancers, myocardial ischemia, renal and hepatic injury.



- **Epigenetic role
in medicine &
Nephrology**

- **Can
epigenetics be
manipulated?**

Full Reviews

Epigenetics: a new way to look at kidney diseases

Pazit Beckerman, Yi-An Ko and Katalin Susztak

Renal Electrolyte and Hypertension Division, Department of Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

Editorial Review

Epigenetics—a helpful tool to better understand processes in clinical nephrology?

Peter Stenvinkel¹ and Tomas J. Ekström²

¹Division of Renal Medicine, Department of Clinical Science, Intervention and Technology and ²Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden

Renal kallikrein excretion and epigenetics in human acute kidney injury: Expression, mechanisms and consequences

[Sun Woo Kang](#),^{#1} [Pei-an Betty Shih](#),^{#2} [Roy O Mathew](#),^{#3} [Manjula Mahata](#),² [Nilima Biswas](#),² [Fangwen Rao](#),² [Liyang Yan](#),⁴ [Josee Bouchard](#),⁵ [Rakesh Malhotra](#),⁶ [Ashita Tolwani](#),⁷ [Srikrishna Khandrika](#),⁶ [Ravindra L Mehta](#),⁶ and [Daniel T O'Connor](#)^{2,6}

Therapeutic use of miRNA antisense may be beneficial, if given early enough, to ameliorate or even stop further injury in AKI and this has been proved in AKI induced by I/P injury in mice.

CKD



Nephrol Dial Transplant (2014) 29: i1–i8

doi: 10.1093/ndt/gft361

Advance Access publication 17 September 2013

ndt
Nephrology Dialysis Transplantation

Full Reviews

Evidence for the involvement of epigenetics in the progression of renal fibrogenesis

Björn Tampe and Michael Zeisberg

Department of Nephrology and Rheumatology, Göttingen University Medical Center, Georg August University, Göttingen, Germany



- **HISTONE MODIFICATIONS**

- histone acetylation has been best studied in the context of CKD, because histone acetylation can be interfered with by using pharmacological inhibitors of histone deacetylases (**HDACs**) reducing fibrosis.

Van Beneden K, et al. 2013

- **CPG METHYLATION**

- RASAL1 encodes for In experimental kidney injury, acute renal damage and chronic progressive fibrosis are associated with transcriptional repression of Rasal1.
- While spontaneous kidney regeneration after acute injury is associated with normalized Rasal1 expression, Rasal1 expression remains silenced in chronic progressive fibrosis due to Rasal1 hypermethylation.

Bechtel W, et al. 2010



- **DNA HYDROXYMETHYLATION**

- In the context of kidney fibrosis, the role of endogenous DNA demethylation mechanisms in the homeostasis of epigenetic modifications has not been described yet.

Ficz G, et al. 2011

- **DNA METHYLTRANSFERASES**

- As hypermethylation can be observed in kidney fibrosis associated with an increase in DNMT1, these mice show ameliorated aberrant promoter methylation.

Bechtel W, et al. 2010

Table 3. Studies of pharmacological modulation of the epigenome in experimental kidney fibrosis

| Name | Experimental model | Effect |
|-----------------------|--|------------------------------|
| 5-Azacytidine | Nephrotoxic serum nephritis [59] | DNA demethylation |
| 5-Aza-2-deoxycytidine | Uninephrectomy-induced glomerulopathy [88] | <i>Klotho</i> demethylation |
| Dexmedetomidine | Sepsis-induced kidney injury [17] | BMP7 induction |
| | Radiocontrast-induced nephropathy [89] | Decreased tubular necrosis |
| | Ischaemia-reperfusion injury [90] | JAK/STAT inhibition |
| MS-275 | Unilateral ureteral obstruction [20] | TGF-beta1/EGFR inhibition |
| Phenylbutyrate | Streptozotocin-induced diabetic nephropathy [86] | ER stress/p-JNK inhibition |
| Trichostatin A | Doxorubicine-induced nephropathy [21] | Less macrophage infiltration |
| | Unilateral ureteral obstruction [16, 22] | Caspase-3 inhibition |
| | TGF-beta1-induced nephropathy [23] | TGF-beta1/ROS inhibition |
| | Streptozotocin-induced diabetic nephropathy [23] | TGF-beta1/ROS inhibition |
| | Nephrotoxic serum nephritis [91] | BMP7 induction |
| Tubacin | Polycystic kidney disease [24] | EGFR inhibition |
| Valproic acid | Doxorubicine-induced nephropathy [21] | Less macrophage infiltration |
| | TGF-beta1-induced nephropathy [23] | TGF-beta1/ROS inhibition |
| | Streptozotocin-induced diabetic nephropathy [23] | TGF-beta1/ROS inhibition |

Table 2. Clinical trials of pharmacological erasure of aberrant methylation listed by the US National Institutes of Health

| Name | Target | # Clinical trials | Disease |
|---------------|--------------------------------|-------------------|--|
| 5-Azacytidine | DNMTs DNA/RNA incorporation | 243 | Carcinomas Graft-versus-host disease Leukaemias Lymphomas Sarcomas |
| Decitabine | DNMTs DNA/RNA incorporation | 132 | Carcinomas Leukaemias Lymphomas Sarcomas |
| Hydralazine | DNMTs | 30 | Carcinomas Hypertension Leukaemias |

Björn Tampe and Michael Zeisberg, 2013



- **Dialysis patients**
- with renal neoplasm showed evidence of DNA hypermethylation of various genes compared to renal neoplasm cases with normal renal function, it appears that CKD and/or the dialysis procedure per se promotes hypermethylation.
- in the uraemic milieu DNA hypermethylation causes silencing of erythropoietin expression

Yin H, Blanchard KL. 2000

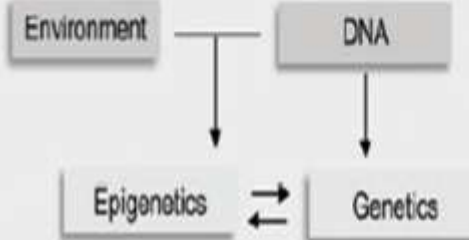


Can epigenetics be manipulated?

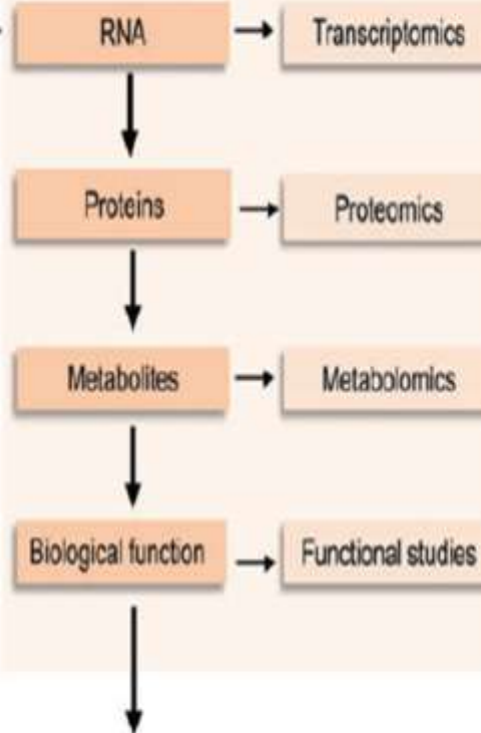
- In theory, epigenetic drugs could possess higher therapeutic potential and much lower rate of adverse effects in comparison to current treatments, such as DNA methylation inhibitors and histone deacetylase inhibitors, exist at various stages of development.
- Although promising results have been reported, major concerns include ***(i.e. lack of target specificity)*** as well as their transient and long term effects.

Take Home Message

I. Genetic and epigenetic association studies



II. Translation into biological knowledge



III. Clinical implications

Diagnostics and prognostics

- Genetic dissection of disease phenotypes
- Risk prediction

Interventions and therapeutics

- Personalized therapy
- Genotype-guided lifestyle interventions
- Pharmacogenomics
- Epigenetic drugs

Kidney disease phenotype and progression

PUGH



*'It's all your fault,
dad - terrible genes'*

